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Comments: ***Proposed claim amendment (do not enter at this point)***

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"Methods for Detecting Contamination in Molecular Diagnostics Using PCR"

U.S.S.N 09/870,729

Filed May 30, 2001 (Atty. docket No.: EXT-010CN)

Proposed claim Amendment [DO NOT ENTER]

1-15. (Canceled)

16. (Amended) A method for detecting contamination by an amplicon from a previous amplification reaction, said method comprising the steps of:

conducting a control nucleic acid amplification reaction in a sample comprising a nucleic acid template, using at least one primer that is capable of amplifying a detection sequence but not said template, said detection sequence having been incorporated in an amplicon of a previous amplification reaction conducted in a different sample using at least one chimeric primer comprising said detection sequence at a 5' end of said at least one chimeric primer; and

determining whether said sample has been contaminated by said previous amplification reaction by determining whether said control reaction produces an amplicon.

17. The method of claim 16, wherein said at least one primer in said control reaction is not complementary to any contiguous nucleic acid sequence in said template.

18. The method of claim 16, wherein said at least one primer in said control reaction is substantially complementary to said detection sequence.

19. The method of claim 16, wherein said at least one primer in said control reaction is substantially identical to said detection sequence.

20. The method of claim 16, wherein said at least one primer in said control reaction further comprises an additional sequence 3' to said detection sequence, said additional sequence being specific for a target in said previous amplification reaction.

21. The method of claim 16, wherein said detection sequence is about 20 nucleotides.

22. The method of claim 16, wherein said nucleic acid comprises DNA.

23. The method of claim 16, wherein at least one of said amplification reactions is selected from the group consisting of PCR, quantitative PCR, and reverse-transcriptase PCR.

24. The method of claim 16, wherein said determination step comprises using a sequence-specific nucleic acid probe to capture said amplicon of said control reaction.

25. The method of claim 16, wherein said sample comprises a heterogeneous population of nucleic acids.

26. The method of claim 25, wherein said sample comprises a stool sample.

27. The method of claim 25, wherein said sample comprises a blood sample.

28. (Amended) A method for detecting contamination by an amplicon from a previous sample, said method comprising the steps of:

conducting an amplification reaction in a first nucleic acid sample, using at least one chimeric primer comprising a first portion that hybridizes with at least a portion of a target nucleic acid, the amplification of which is desired, and a second, contamination detection portion that does not hybridize with said target nucleic acid;

conducting a control amplification reaction in a second nucleic acid sample different from said first nucleic acid sample, using at least one primer to amplify specifically said contamination detection portion of said chimeric primer; and

determining whether said second sample has been contaminated by an amplicon from said first sample by determining whether said control reaction produces an amplicon.

29. The method of claim 28, wherein said second portion is 5' to said first portion in each of said at least one chimeric primers.

30. The method of claim 28, wherein said at least one primer in said control reaction is not complementary to any contiguous nucleic acid sequence in any target nucleic acid in said second sample.

31. The method of claim 28, wherein said at least one primer used in said control reaction is substantially complementary to said contamination detection portion.

32. The method of claim 28, wherein said at least one primer used in said control reaction is substantially identical to said contamination detection portion.

33. The method of claim 28, wherein at least one of said amplification reactions is selected from the group consisting of PCR, quantitative PCR, and reverse-transcriptase PCR.

34. The method of claim 28, wherein said samples comprise a heterogeneous population of nucleic acids.

35. The method of claim 34, wherein said samples comprise a stool sample.

36. The method of claim 34, wherein said samples comprise a blood sample.

37. The method of claim 28, wherein said contamination detection portion is about 20 nucleotides.

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